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OM protein - protein search, using sw model

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Run on:      October 1, 2008, 12:46:15 ; Search time 829 Seconds
              (without alignments)
              1085.529 Million cell updates/sec
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```
Title:          US-10-552-515-1
Perfect score:  4950
Sequence:       1 MRMAATAWAGLQGPPLPTLC.....SELSSHWTPFTVPKASQLQQ 933
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Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 4190237 seqs, 964526986 residues

Total number of hits satisfying chosen parameters: 4190237

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
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Database :      Published_Applications_AA_Main:*
1:   /ABSS/Data/CRF/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2:   /ABSS/Data/CRF/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
3:   /ABSS/Data/CRF/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
4:   /ABSS/Data/CRF/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
5:   /ABSS/Data/CRF/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
6:   /ABSS/Data/CRF/ptodata/2/pubpaa/US11A_PUBCOMB.pep:*
7:   /ABSS/Data/CRF/ptodata/2/pubpaa/US11B_PUBCOMB.pep:*
8:   /ABSS/Data/CRF/ptodata/2/pubpaa/US12_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result		%					
No.	Score	Query Match	Length	DB	ID	Description	
1	4950	100.0	933	5	US-10-552-515-1	Sequence 1, Appli	
2	4531.5	91.5	885	7	US-11-599-845A-700	Sequence 700, App	
3	4364.5	88.2	843	7	US-11-599-845A-698	Sequence 698, App	
4	3736	75.5	898	5	US-10-450-763-45847	Sequence 45847, A	
5	1531.5	30.9	920	4	US-10-104-047-2574	Sequence 2574, Ap	
6	1531.5	30.9	920	6	US-11-072-512-2574	Sequence 2574, Ap	
7	1527.5	30.9	981	6	US-11-582-861-10841	Sequence 10841, A	
8	1511	30.5	1046	6	US-11-582-861-9875	Sequence 9875, Ap	
9	1508	30.5	981	6	US-11-443-428A-801153	Sequence 801153,	
10	1488	30.1	960	6	US-11-177-894-7	Sequence 7, Appli	
11	1479.5	29.9	840	6	US-11-177-894-11	Sequence 11, Appl	
12	1464	29.6	999	6	US-11-443-428A-774192	Sequence 774192,	
13	1445	29.2	1219	6	US-11-097-143-15228	Sequence 15228, A	
14	1417	28.6	800	6	US-11-443-428A-739452	Sequence 739452,	
15	1417	28.6	800	6	US-11-443-428A-739454	Sequence 739454,	
16	1416	28.6	853	6	US-11-443-428A-739456	Sequence 739456,	
17	1402.5	28.3	910	5	US-10-484-148-14	Sequence 14, Appl	
18	1386	28.0	891	6	US-11-582-861-10193	Sequence 10193, A	
19	1369.5	27.7	1075	6	US-11-097-143-24771	Sequence 24771, A	
20	1367.5	27.6	712	6	US-11-177-894-10	Sequence 10, Appl	
21	1199.5	24.2	1058	6	US-11-097-143-21858	Sequence 21858, A	
22	1154	23.3	596	4	US-10-104-047-2541	Sequence 2541, Ap	
23	1154	23.3	596	6	US-11-072-512-2541	Sequence 2541, Ap	
24	1061.5	21.4	594	5	US-10-631-467-681	Sequence 681, App	
25	1061.5	21.4	594	5	US-10-529-348-1242	Sequence 1242, Ap	
26	1061.5	21.4	594	5	US-10-917-503-10953	Sequence 10953, A	
27	1061.5	21.4	594	6	US-11-177-894-8	Sequence 8, Appli	
28	1056.5	21.3	825	6	US-11-443-428A-1026041	Sequence 1026041,	
29	1037.5	21.0	782	4	US-10-066-543-1424	Sequence 1424, Ap	
30	1037.5	21.0	793	6	US-11-443-428A-1026033	Sequence 1026033,	
31	912.5	18.4	475	4	US-10-104-047-3116	Sequence 3116, Ap	
32	912.5	18.4	475	6	US-11-072-512-3116	Sequence 3116, Ap	
33	909	18.4	756	5	US-10-692-382-446	Sequence 446, App	
34	905	18.3	642	4	US-10-108-260A-4483	Sequence 4483, Ap	
35	905	18.3	642	6	US-11-177-894-9	Sequence 9, Appli	
36	905	18.3	642	6	US-11-293-697-4483	Sequence 4483, Ap	
37	886	17.9	573	6	US-11-443-428A-774194	Sequence 774194,	
38	881.5	17.8	550	6	US-11-443-428A-774193	Sequence 774193,	
39	829	16.7	631	6	US-11-443-428A-739453	Sequence 739453,	
40	819.5	16.6	443	4	US-10-264-049-2917	Sequence 2917, Ap	
41	817.5	16.5	179	5	US-10-495-663-1	Sequence 1, Appli	
42	814.5	16.5	853	6	US-11-443-428A-1026043	Sequence 1026043,	
43	784.5	15.8	390	4	US-10-264-237-2758	Sequence 2758, Ap	
44	735	14.8	139	3	US-09-957-708-31	Sequence 31, Appl	
45	735	14.8	139	6	US-11-230-251-31	Sequence 31, Appl	

## ALIGNMENTS

RESULT 1

US-10-552-515-1

; Sequence 1, Application US/10552515  
; Publication No. US20060194204A1  
; GENERAL INFORMATION:  
; APPLICANT: The Government of the United States of America as  
; APPLICANT: represented by the Secretary of the Department of Health and  
; APPLICANT: Human Services  
; APPLICANT: Bera, Tapan K.  
; APPLICANT: Pastan, Ira H.  
; APPLICANT: Lee, Byungkook  
; TITLE OF INVENTION: GENE EXPRESSED IN PROSTATE CANCER AND METHODS OF USE  
; FILE REFERENCE: 4239-68223-02  
; CURRENT APPLICATION NUMBER: US/10/552,515  
; CURRENT FILING DATE: 2005-10-06  
; PRIOR APPLICATION NUMBER: PCT/US2004/10588  
; PRIOR FILING DATE: 2004-04-05  
; PRIOR APPLICATION NUMBER: 60/461,399  
; PRIOR FILING DATE: 2003-04-08  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 1  
; LENGTH: 933  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Splice Variant-Novel Gene Expressed in Prostate

US-10-552-515-1

Query Match 100.0%; Score 4950; DB 5; Length 933;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 933; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MRMAATAWAGLQGPPLPTLCPAVRTGLYCRDQAHAERWAMTSETSSGSHCARSRMLRRRA	60
Db	1	MRMAATAWAGLQGPPLPTLCPAVRTGLYCRDQAHAERWAMTSETSSGSHCARSRMLRRRA	60
Qy	61	QEEDSTVLIDVSPPEAEKRGSYGSTAHASEPGGQQAACRAGSPAKPRIADFVLVWEEDL	120
Db	61	QEEDSTVLIDVSPPEAEKRGSYGSTAHASEPGGQQAACRAGSPAKPRIADFVLVWEEDL	120
Qy	121	KLDRQQDSAARDRTDMHRTWRETFLDNLRAAGLCVDQQDVQDGNTTVHYALLSASWAVLC	180
Db	121	KLDRQQDSAARDRTDMHRTWRETFLDNLRAAGLCVDQQDVQDGNTTVHYALLSASWAVLC	180
Qy	181	YYAEDLRLKLPLQELPNQASNWSAGLLAWLGIPNVLLEVPDVPPEYYSCRFRVKNLPRF	240
Db	181	YYAEDLRLKLPLQELPNQASNWSAGLLAWLGIPNVLLEVPDVPPEYYSCRFRVKNLPRF	240
Qy	241	LGSDNQDTFFTSTKRHQILFEILAKTPYGHEKKNLLGIHQLLAEGVLSAAFPLHDGPFKT	300
Db	241	LGSDNQDTFFTSTKRHQILFEILAKTPYGHEKKNLLGIHQLLAEGVLSAAFPLHDGPFKT	300

Qy	301	PPEGPQAPRLNQVLFQHWARWGKWNKYQPLDHVRRYFGEKVALYFAWLGFYTGWLLPA	360
Db	301	PPEGPQAPRLNQVLFQHWARWGKWNKYQPLDHVRRYFGEKVALYFAWLGFYTGWLLPA	360
Qy	361	AVVGTLVFLVGCFLVFSDIPTQELCGSKDSFEMCPLCLDCPFWLLSSACALAQAGRLFDH	420
Db	361	AVVGTLVFLVGCFLVFSDIPTQELCGSKDSFEMCPLCLDCPFWLLSSACALAQAGRLFDH	420
Qy	421	GGTVFFSLFMALWAVLLLEYWKRKSATLAYRWDCSDYEDTEERPRPQFAASAPMTAPNPI	480
Db	421	GGTVFFSLFMALWAVLLLEYWKRKSATLAYRWDCSDYEDTEERPRPQFAASAPMTAPNPI	480
Qy	481	TGEDEPYFPERSRARRMLAGSVVIVVMVAVVVMCLVSIILYRAIMAIIVSRSGNTLLAAW	540
Db	481	TGEDEPYFPERSRARRMLAGSVVIVVMVAVVVMCLVSIILYRAIMAIIVSRSGNTLLAAW	540
Qy	541	ASRIASLTGSVVNLVFIILSKIYVSLAHVLTRWEMHRTQTKFEDAFTLKVFIQFVNFI	600
Db	541	ASRIASLTGSVVNLVFIILSKIYVSLAHVLTRWEMHRTQTKFEDAFTLKVFIQFVNFI	600
Qy	601	SSPVYIAFFKGRFVGYPGNYHTLFGVRNEECAAGGCLIELAQELLVIMVGKQVINNMQEV	660
Db	601	SSPVYIAFFKGRFVGYPGNYHTLFGVRNEECAAGGCLIELAQELLVIMVGKQVINNMQEV	660
Qy	661	LIPKLKGWWQKFRRLRSKKRKAGASAGASQGPWEDDYELVPCEGLFDEYLEMVLQFGFVTI	720
Db	661	LIPKLKGWWQKFRRLRSKKRKAGASAGASQGPWEDDYELVPCEGLFDEYLEMVLQFGFVTI	720
Qy	721	FVAACPLAPLFAALLNNWVEIRLDARKFVCEYRRPVAERAQDIGIWFHILAGLTHLAVISN	780
Db	721	FVAACPLAPLFAALLNNWVEIRLDARKFVCEYRRPVAERAQDIGIWFHILAGLTHLAVISN	780
Qy	781	AFLLAFFSSDFLPRAYYRWTRAHDLRGFLNFTTLARAPSSFAAAHNRTCERYAFRDDDGHYS	840
Db	781	AFLLAFFSSDFLPRAYYRWTRAHDLRGFLNFTTLARAPSSFAAAHNRTCERYAFRDDDGHYS	840
Qy	841	QTYWNLLAIRLAFVIVFEHVVSFVGRLDLLVDPDIPESVEIKVKREYYLAKQALAEVNL	900
Db	841	QTYWNLLAIRLAFVIVFEHVVSFVGRLDLLVDPDIPESVEIKVKREYYLAKQALAEVNL	900
Qy	901	FGTNGTKDEQPKGSELSSHWPFTVTPKASQLQQ	933
Db	901	FGTNGTKDEQPKGSELSSHWPFTVTPKASQLQQ	933

## RESULT 2

US-11-599-845A-700

; Sequence 700, Application US/11599845A

; Publication No. US20080025981A1

; GENERAL INFORMATION:

; APPLICANT: Young, Paul E.

; APPLICANT: Ebner, Reinhard

; APPLICANT: Weaver, Zoe

; APPLICANT: Strovel, Jeffrey W.

; APPLICANT: Horrigan, Stephen K.  
; APPLICANT: Shea, Martin  
; APPLICANT: Weigle, Bernd  
; APPLICANT: Rieger, Michael  
; APPLICANT: Rick, Jennifer A.  
; APPLICANT: Cain, Colyn B.  
; TITLE OF INVENTION: Cancer-linked Genes as Target for Chemotherapy  
; FILE REFERENCE: 689290-273  
; CURRENT APPLICATION NUMBER: US/11/599,845A  
; CURRENT FILING DATE: 2006-11-15  
; PRIOR APPLICATION NUMBER: 10/585,466  
; PRIOR FILING DATE: 2005-01-04  
; PRIOR APPLICATION NUMBER: PCT/US2005/000040  
; PRIOR FILING DATE: 2005-01-04  
; PRIOR APPLICATION NUMBER: 10/583,832  
; PRIOR FILING DATE: 2004-12-16  
; PRIOR APPLICATION NUMBER: PCT/US2004/42406  
; PRIOR FILING DATE: 2004-12-16  
; PRIOR APPLICATION NUMBER: 10/575,337  
; PRIOR FILING DATE: 2004-10-07  
; PRIOR APPLICATION NUMBER: PCT/US2004/33072  
; PRIOR FILING DATE: 2004-10-07  
; PRIOR APPLICATION NUMBER: 10/540,310  
; PRIOR FILING DATE: 2003-12-19  
; PRIOR APPLICATION NUMBER: PCT/US2003/40710  
; PRIOR FILING DATE: 2003-12-19  
; PRIOR APPLICATION NUMBER: 10/518,039  
; PRIOR FILING DATE: 2003-06-10  
; PRIOR APPLICATION NUMBER: PCT/US2003/19741  
; PRIOR FILING DATE: 2003-06-10  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 769  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 700  
; LENGTH: 885  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-599-845A-700

Query Match 91.5%; Score 4531.5; DB 7; Length 885;  
Best Local Similarity 99.7%; Pred. No. 0;  
Matches 855; Conservative 0; Mismatches 0; Indels 3; Gaps 2;

Qy	1	MRMAATAWAGLQGPPLPTLCPAVRTGLYCRDQAHAERWAMTSETSSGSHCARSRMLRRRA	60
Db	5	MRMAATAWAGLQGPPLPTLCPAVRTGLYCRDQAHAERWAMTSETSSGSHCA--RMLRRRA	62
Qy	61	QEEDSTVLIDVSPPEAEKRGSYGSTAHASEPGGQQAACRAGSPAKPRIADFLVWWEEDL	120
Db	63	QEEDSTVLIDVSPPEAEKRGSYGSTAHASEPGGQQAACRAGSPAKPRI-DFVLVWWEEDL	121
Qy	121	KLDRQQDSAARDRTDMHRTWRETFLDNLRAAGLCVDQQDVQDGNTTVHYALLSASWAVLC	180
Db	122	KLDRQQDSAARDRTDMHRTWRETFLDNLRAAGLCVDQQDVQDGNTTVHYALLSASWAVLC	181

Qy	181	YYAEDLRLKLPQELPNQASNWSAGLLAWLGIPNVLLEVPDVPPEYYSCRFRVKNLPRF	240
Db	182	YYAEDLRLKLPQELPNQASNWSAGLLAWLGIPNVLLEVPDVPPEYYSCRFRVKNLPRF	241
Qy	241	LGSDNQDTFFTSTKRHQILFEILAKTPYGHEKKNLLGIHQLLAEGVLSAAFPLHDGPFKT	300
Db	242	LGSDNQDTFFTSTKRHQILFEILAKTPYGHEKKNLLGIHQLLAEGVLSAAFPLHDGPFKT	301
Qy	301	PPEGPQAPRLNQEQVLFQHWARWGKWNKYQPLDHVRRYFGEKVALYFAWLGFYTGWLLPA	360
Db	302	PPEGPQAPRLNQEQVLFQHWARWGKWNKYQPLDHVRRYFGEKVALYFAWLGFYTGWLLPA	361
Qy	361	AVVGTLVFLVGCFLVFSDIPTQELCGSKDSFEMCPLCLDCPFWLLSSACALAQAGRLFDH	420
Db	362	AVVGTLVFLVGCFLVFSDIPTQELCGSKDSFEMCPLCLDCPFWLLSSACALAQAGRLFDH	421
Qy	421	GGTVFFSLFMALWAVLLLEYWKRKSATLAYRWDCSDYEDTEERPRPQFAASAPMTAPNPI	480
Db	422	GGTVFFSLFMALWAVLLLEYWKRKSATLAYRWDCSDYEDTEERPRPQFAASAPMTAPNPI	481
Qy	481	TGEDEPYFPERSRARRMLAGSVVIVVMVAVVVMCLVSIILYRAIMAIIVSRSGNTLLAAW	540
Db	482	TGEDEPYFPERSRARRMLAGSVVIVVMVAVVVMCLVSIILYRAIMAIIVSRSGNTLLAAW	541
Qy	541	ASRIASLTGSVVNLVFIILSKIYVSLAHVLTRWEMHRTQTKFEDAFTLKVFIFQFVNIFY	600
Db	542	ASRIASLTGSVVNLVFIILSKIYVSLAHVLTRWEMHRTQTKFEDAFTLKVFIFQFVNIFY	601
Qy	601	SSPVYIAFFKGRFVGYPGNYHTLFGVRNEECAAGGCLIELAQELLVIMVGKQVINNMQEV	660
Db	602	SSPVYIAFFKGRFVGYPGNYHTLFGVRNEECAAGGCLIELAQELLVIMVGKQVINNMQEV	661
Qy	661	LIPKLKGWWQKFRLRSKKRKAGASAGASQGPWEDDYELVPCEGLFDEYLEMVLQFGFVTI	720
Db	662	LIPKLKGWWQKFRLRSKKRKAGASAGASQGPWEDDYELVPCEGLFDEYLEMVLQFGFVTI	721
Qy	721	FVAACPLAPLFAALLNNWVEIRLDARKFVCEYRRPVAERAQDIGIWFHILAGLTHLAVISN	780
Db	722	FVAACPLAPLFAALLNNWVEIRLDARKFVCEYRRPVAERAQDIGIWFHILAGLTHLAVISN	781
Qy	781	AFLLAFFSSDFLPRAYYRWTRAHDLRGFLNFTTLARAPSSFAAAHNRTCERYAFRDDDGHYS	840
Db	782	AFLLAFFSSDFLPRAYYRWTRAHDLRGFLNFTTLARAPSSFAAAHNRTCERYAFRDDDGHYS	841
Qy	841	QTYWNLLAIRLAFVIVFE	858
Db	842	QTYWNLLAIRLAFVIVFE	859

RESULT 3

US-11-599-845A-698

; Sequence 698, Application US/11599845A

; Publication No. US20080025981A1

Query Match 88.2%; Score 4364.5; DB 7; Length 843;  
Best Local Similarity 99.6%; Pred. No. 0;  
Matches 824; Conservative 0; Mismatches 0; Indels 3; Gaps 2;

[illegible]

Db	63	QEEDSTVLIDVSPPEAEKRGSYGSTAHASEPGGQQAACRAGSPAKPRI-DFVLVWEEDL	121
Qy	121	KLDRQQDSAARDRTDMHRTWRETFLDNLRAAGLCVDQQDVQDGNTTVHYALLSASWAVLC	180
Db	122	KLDRQQDSAARDRTDMHRTWRETFLDNLRAAGLCVDQQDVQDGNTTVHYALLSASWAVLC	181
Qy	181	YYAEDLRLKLPLQELPNQASNWSAGLLAWLGIPNVLLEVPDVPPEYYSCRFRVKNLPRF	240
Db	182	YYAEDLRLKLPLQELPNQASNWSAGLLAWLGIPNVLLEVPDVPPEYYSCRFRVKNLPRF	241
Qy	241	LGSDNQDTFFTSTKRHQILFEILAKTPYGHEKKNLLGIHQLLAEGVLSAAFPLHDGPFKT	300
Db	242	LGSDNQDTFFTSTKRHQILFEILAKTPYGHEKKNLLGIHQLLAEGVLSAAFPLHDGPFKT	301
Qy	301	PPEGPQAPRLNQRQVLFQHWARWGKWNKYQPLDHVRRYFGEKVALYFAWLGFYTGWLLPA	360
Db	302	PPEGPQAPRLNQRQVLFQHWARWGKWNKYQPLDHVRRYFGEKVALYFAWLGFYTGWLLPA	361
Qy	361	AVVGTLVFLVGCFLVFSDIPTQELCGSKDSFEMCPLCLDCPFWLLSSACALAQAGRLFDH	420
Db	362	AVVGTLVFLVGCFLVFSDIPTQELCGSKDSFEMCPLCLDCPFWLLSSACALAQAGRLFDH	421
Qy	421	GGTVFFSLFMALWAVLLLEYWKRKSATLAYRWDCSDYEDTEERPRPQFAASAPMTAPNPI	480
Db	422	GGTVFFSLFMALWAVLLLEYWKRKSATLAYRWDCSDYEDTEERPRPQFAASAPMTAPNPI	481
Qy	481	TGEDEPYFPERSRARRMLAGSVVIVVMVAVVVMCLVSIILYRAIMAIVVSRSNTLLAAW	540
Db	482	TGEDEPYFPERSRARRMLAGSVVIVVMVAVVVMCLVSIILYRAIMAIVVSRSNTLLAAW	541
Qy	541	ASRIASLTGSVVNLVFIILSKIYVSLAHVLTRWEMHRTQTKFEDAFTLKVFIQFVNIFY	600
Db	542	ASRIASLTGSVVNLVFIILSKIYVSLAHVLTRWEMHRTQTKFEDAFTLKVFIQFVNIFY	601
Qy	601	SSPVYIAFFKGRFVGYPGNYHTLFGVRNEECAAGGCLIELAQELLVIMVGKQVINNMQEV	660
Db	602	SSPVYIAFFKGRFVGYPGNYHTLFGVRNEECAAGGCLIELAQELLVIMVGKQVINNMQEV	661
Qy	661	LIPKLKGWWQKFRRLRSKKRKAGASAGASQGPWEDDYELVPCEGLFDEYLEMVLQFGFVTI	720
Db	662	LIPKLKGWWQKFRRLRSKKRKAGASAGASQGPWEDDYELVPCEGLFDEYLEMVLQFGFVTI	721
Qy	721	FVAACPLAPLFAALLNNWVEIRLDARKFVCEYRRPVAERAQDIGIWFHILAGLTHLAVISN	780
Db	722	FVAACPLAPLFAALLNNWVEIRLDARKFVCEYRRPVAERAQDIGIWFHILAGLTHLAVISN	781
Qy	781	AFLLAFFSSDFLPRAYYRWTRAHDLRGFLNFTLARAPSSFAAAHNRTC	827
Db	782	AFLLAFFSSDFLPRAYYRWTRAHDLRGFLNFTLARAPSSFAAAHNRTC	828



Query Match 75.5%; Score 3736; DB 5; Length 898;  
Best Local Similarity 82.3%; Pred. No. 0;  
Matches 727; Conservative 4; Mismatches 16; Indels 136; Gaps 6;

Qy	1	MRMAATAWAGLQGPPLPTLCPAVRTGLYCRDQAHAER-----	37
Db	1	MRMAATAWAGLQGPPLPTLCPAVRTGLYCRDQAHAERATDVLLAPFCQPKTRSHGTCPP	60
Qy	38	-----W---AMTSETS-----SG	47
		:	
Db	61	TERDPRGEGSTEYPGRVDGIQGWGTRALTGWTDRLLCQACQTLPPRHWFLLPGARGWLGG	120
Qy	48	SHCA-----RSRMLRRAQEEDSTVLIDVSPPEAEKRGSYGSTAH	87
		:	
Db	121	SPCAHGQESLPSQPSPILLRVESVKSRLRRAQEEDSTVLIDVSPPEAEKRGSYGSTAH	180
Qy	88	ASEPGGQQAACRAGSPAKPRIADFLVWVEEDLKLDRQQDSAARDRTDMHRTWRETFLDN	147
Db	181	ASEPGGQQAACRAGSPAKPRIADFLVWVEEDLKLDRQQDSAARDRTDMHRTWRETFLDN	240
Qy	148	LRAAGLCVDQQDVQDGNTTVHYALLSASWAVLCYYAEDLRLKLPLQELPNQASNWSAGLL	207
		:   :	
Db	241	LRAAGLCVDQQDVQDGNTTVHYALLSASWAVLCYYAEDLRLKLPLQDYPTRPPTGRPACC	300
Qy	208	AWLGIPNVLLEVPDVPPEYYSCRFRVNKLPRFLGSDNQDTFFTSTKRHQILFEILAKTP	267
Db	301	AWLGIPNVLLEVPDVPPEYYSCRFRVNKLPRFLGSDNQDTFFTSTKRHQILFEILAKTP	360
Qy	268	YGHEKKNLLGIHQLLAEGVLSAAFPLHDGPFKTPPEGPQAPRLNQRVLFQHWARWGKWN	327
Db	361	YGHEKKNLLGIHQLLAEGVLSAAFPLHDGPFKTPPEGPQAPRLNQRVLFQHWARWGKWN	420
Qy	328	KYQPLDHVRRYFGEKVLYFAWLGFYTGWLLPAAVVGTLVFLVGCFLVFSDIPTQELCGS	387

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      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      421 KYQPLDHVRRYFGEKVALYFAWLGFYTGWLLPAAVVGTLVFLVGCFLVFSDIPTQELCGS 480
Qy      388 KDSFEMCPLCLDCPFWLLSSACALAQ----AGRLFDHGGTVFFSLFMALWAVLLLEYWKR 443
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      481 KDSFEMCPLCLDCPFWLLSSACALAQVREEAGRLFDHGGTVFFSLFMALWAVLLLEYWKR 540
Qy      444 KSATLAYRWDCSDYEDTEERPRPQFAASAPMTAPNPITGEDEPYFPERSRARRMLAGSVV 503
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      541 KSATLAYRWDCSDYEDTEERPRPQFAASAPMTAPNPITGEDEPYFPERSRARRMLAGSVV 600
Qy      504 IVVMVAVVVMCLVSIILYRAIMAIIVVSRSGNTLLAAWASRIASLTGSVVNLVFILILSKI 563
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      601 IVVMVAVVVMCLVSIILYRAIMAIIVVSRSGNTLLAAWASRIASLTGSVVNLVFILILSKI 660
Qy      564 YVSLAHVLTRWEMHRTQTKFEDAFTLKVFIFQFVNFYSSPVYIAFFKGRFVGYPGNYHTL 623
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      661 YVSLAHVLTRWEMHRTQTKFEDAFTLKVFIFQFVNFYSSPVYIAFFKGRFVGYPGNYHTL 720
Qy      624 FGVRNEECAAGGCLIELAQELLVIMVGKQVINNMQEVLPKLKGWWQKFRLRSKKRKAGA 683
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      721 FGVRNEECAAGGCLIELAQELLVIMVGKQVINNMQEVLPKLKGWWQKFRLRSKKRKAGA 780
Qy      684 SAGASQGPWEDDYELVPCEGLFDEYLEM----- 711
      |||||||||||||||||||||||||||||||||||
Db      781 SAGASQGPWEDDYELVPCEGLFDEYLEMGAGFCPNACPELVPPELPEPEKARDQPEARSAG 840
Qy      712 -----VLQFGFVTIFVAACPLAPLFALLNNWVEIRLDARKE 747
      |||||||||||||||||||||||||||||||||||
Db      841 QDSRPEAVLQFGFVTIFVAACPLAPLFALLNNWVEIRLDARKE 883
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RESULT 5

US-10-104-047-2574

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; Sequence 2574, Application US/10104047
; Publication No. US20030236392A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20030236392A1e1 full length cDNA
; FILE REFERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2574
; LENGTH: 920
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-104-047-2574
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Query Match 30.9%; Score 1531.5; DB 4; Length 920;  
Best Local Similarity 37.9%; Pred. No. 1.9e-138;

Matches 360; Conservative 168; Mismatches 316; Indels 105; Gaps 29;	
Qy	44 TSSGSHCARSRMLRRRAQEEDSTVLID----VSPPEAE-----KRGSYGST---AHASEP 91
Db	4 SSSGITNGKTKVFHPVA--KDVNILFDELEAVSSPCKDDDSLHHPGNLTSTSDDASRLEA 61
Qy	92 GGQQAACRAGS-----PAKPRIADFVLVWEEDLKLDRQQDSAARDRTDMHRTWRETFLD 146
Db	62 GGETVPERNKSNGLYFRDGKCRI-DYILVYRK-----SNPQTEK---REVFER 105
Qy	147 NLRAAGLCVDQQDVQDGNTTVHYALLSASWAVLCYYAEDLRLKLPLQE---LPNQASNW 202
Db	106 NIRAAGLQMEKESSLI-NSDIIFVKLHAPWEVLGRYAEQMNVRMPFRRKIYYLPRRYKFM 164
Qy	203 S-----AGLLAWLGIPNVLL--EVVPDVPP-EYYSRFRVNKLPRFLGSDNQDTFFTST 253
Db	165 SRIDKQISRLRRWLPKKPMRLDKETLPDLEENDCYTAPFSQQRIHHFI-IHNKETFFNNA 223
Qy	254 KRHQILFEILAKTPYGHEKKNLLGIHQLLAEGVLSAAFPPLHDGPFKTPPEGPQAPRLNQR 313
Db	224 TRSRIVHHILQRIKY-EEGKNKIGLNRLLTNGSYEAAFPPLHEGSYRSKNSIRTHGAENHR 282
Qy	314 QVLFQHWARWGKWNKYQPLDHVRRYFGEKVALYFAWLGFYTGWLLPAAVVGTLVFLVGCF 373
Db	283 HLLYECWASWGVWYKYQPLDLVRRYFGEKIGLYFAWLGWYTGMLFPAAFIGLFVFLYGV 342
Qy	374 LVFSDIPTQELCGSKDSFEMCPLC-LDCPFWLLSSACALAQAGRLFDHGGTVFFSLFMAL 432
Db	343 TLDHSQVSKEVCQATDII-MCPVCDKYCPFMRLSDSCVYAKVTHLFDNGATVFFFAVMAV 401
Qy	433 WAVLLLEYWKRKSATLAYRWDCSDYEDTEERPRPQFAAS-APMTAPNPITGEDEPYFPER 491
Db	402 WATVFLEFWKRRRAVIAYDWDLIDWEEEEEEIRPQFEAKYSKKERMNPISGKPEPYQAF 461
Qy	492 SRARRMLAGSVVIVVMVAVVVMCLVSIILYRAIMAIVVSRSNTLLA-AWA-----SRIA 545
Db	462 DKCSRLIVSASGIFFMICVVIAAVFGIVIVRVTV-----STFAAFKWALIRNNSQVA 514
Qy	546 SLTGSVV--NLVFILILSKIYVSLAHVLTRWEMHRTQTKFEDAFTLKVFIFQFVNFYSSP 603
Db	515 T-TGTAVCINFCIIMLLNVLYEKVALLLTNLEQPRTESEWENSFTLKMFLFQFVNLSST 573
Qy	604 VYIAFFKGRFVGYPGNHYHTLFG-VRNEECAAGGLIELAQELLVIMVGKQVINNMQEVL 662
Db	574 FYIAFFLGRFTGHPGAYLRLINRWRLLEECHPSGCLIDLQMGIIMVLKQTWNNFMELGY 633
Qy	663 PKLKGWWQKFRRLRSKKRKAGASAGASQGPWEDDYELVPCE--GLFDEYLEMVLQFGFVTI 720
Db	634 PLIQNWWR---RKVRQEHGPERKISFPQWEKDYNLQPMNAYGLFDEYLEMILQFGFTTI 690
Qy	721 FVAACPLAPLFAALLNNWVEIRLDARKFVCEYRRPVAERAQDIGIWFHILAGLTHLAVISN 780
Db	691 FVAAFPLAPLLALLNNIIEIRLDAYKFVTQWRRPLASRAKDIGIWIYGILEGIGILSVITN 750

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; Sequence 2574, Application US/11072512
; Publication No. US20060029945A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHIKO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: 084335-0191
; CURRENT APPLICATION NUMBER: US/11/072,512
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: US 60/350,978
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: JP 2001-379298
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2574
; LENGTH: 920
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-072-512-2574

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http://es/ScoreAccessWeb/GetItem.action?AppId=10552...124607\_us-10-552-515-1.rapbm&ItemType=4&startByte=0 (12 of 29)10/10/2008 8:45:58 AM

Matches 360; Conservative 168; Mismatches 316; Indels 105; Gaps 29;	
Qy	44 TSSGSHCARSRMLRRRAQEEDSTVLID----VSPPEAE-----KRGSYGST---AHASEP 91
Db	4 SSSGITNGKTKVFHPVA--KDVNILFDELEAVSSPCKDDDSLHHPGNLTSTSDDASRLEA 61
Qy	92 GGQQAACRAGS-----PAKPRIADFVLVWEEDLKLDRQQDSAARDRTDMHRTWRETFLD 146
Db	62 GGETVPERNKSNGLYFRDGKCRI-DYILVYRK-----SNPQTEK----REVFER 105
Qy	147 NLRAAGLCVDQQDVQDGNTTVHYALLSASWAVLCYYAEDLRLKLPLQE----LPNQASNW 202
Db	106 NIRAAGLQMEKESSLI-NSDIIFVKLHAPWEVLGRYAEQMNVRMPFRRKIYYLPRRYKFM 164
Qy	203 S-----AGLLAWLGIPNVLL--EVVPDVPP-EYYSRFRVNKLPRFLGSDNQDTFFTST 253
Db	165 SRIDKQISRLRRWLPKKPMRLDKETLPDLEENDCYTAPFSQQRIHHFI-IHNKETFFNNA 223
Qy	254 KRHQILFEILAKTPYGHEKKNLLGIHQLLAEGVLSAAFPPLHDGPFKTPPEGPQAPRLNQR 313
Db	224 TRSRIVHHILQRIKY-EEGKNKIGLNRLLTNGSYEAAFPPLHEGSYRSKNSIRTHGAENHR 282
Qy	314 QVLFQHWARWGKWNKYQPLDHVRRYFGEKVALYFAWLGFYTGWLLPAAVVGTLVFLVGCF 373
Db	283 HLLYECWASWGVWYKYQPLDLVRRYFGEKIGLYFAWLGWYTGMLFPAAFIGLFVFLYGV 342
Qy	374 LVFSDIPTQELCGSKDSFEMCPLC-LDCPFWLLSSACALAQAGRLFDHGGTVFFSLFMAL 432
Db	343 TLDHSQVSKEVCQATDII-MCPVCDKYCPFMRLSDSCVYAKVTHLFDNGATVFFFAVMAV 401
Qy	433 WAVLLLEYWKRKSATLAYRWDCSDYEDTEERPRPQFAAS-APMTAPNPITGEDEPYFPER 491
Db	402 WATVFLEFWKRRRAVIAYDWDLIDWEEEEEEIRPQFEAKYSKKERMNPISGKPEPYQAF 461
Qy	492 SRARRMLAGSVVIVVMVAVVVMCLVSIILYRAIMAIVVSRSGNTLLA-AWA-----SRIA 545
Db	462 DKCSRLIVSASGIFFMICVVIAAVFGIVIVRVTV-----STFAAFKWALIRNNSQVA 514
Qy	546 SLTGSVV--NLVFILILSKIYVSLAHVLTRWEMHRTQTKFEDAFTLKVFIFQFVNFYSSP 603
Db	515 T-TGTAVCINFCIIMLLNVLYEKVALLLTNLEQPRTESEWENSFTLKMFLFQFVNLSST 573
Qy	604 VYIAFFKGRFVGYPGNHYHTLFG-VRNEECAAGGLIELAQELLVIMVGKQVINNMQEVL 662
Db	574 FYIAFFLGRFTGHPGAYLRLINRWRLLEECHPSGCLIDLQMGIIMVLKQTWNNFMELGY 633
Qy	663 PKLKGWWQKFRRLRSKKRKAGASAGASQGPWEDDYELVPCE--GLFDEYLEMVLQFGFVTI 720
Db	634 PLIQNWWR---RKVRQEHGPERKISFPQWEKDYNLQPMNAYGLFDEYLEMILQFGFTTI 690
Qy	721 FVAACPLAPLFAALLNNWVEIRLDARKFVCEYRRPVAERAQDIGIWFHILAGLTHLAVISN 780
Db	691 FVAAFPLAPLLALLNNIIEIRLDAYKFVTQWRRPLASRAKDIGIWIYGILEGIGILSVITN 750

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US-11-582-861-10841
; Sequence 10841, Application US/11582861
; Publication No. US20070099251A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Hui
; APPLICANT: Aebersold, Rudolf H.
; TITLE OF INVENTION: TISSUE- AND SERUM-DERIVED GLYCOPROTEINS
; TITLE OF INVENTION: AND METHODS OF THEIR USE
; FILE REFERENCE: 460092.404
; CURRENT APPLICATION NUMBER: US/11/582,861
; CURRENT FILING DATE: 2006-10-17
; PRIOR APPLICATION NUMBER: US 60/728,044
; PRIOR FILING DATE: 2005-10-17
; NUMBER OF SEQ ID NOS: 14918
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10841
; LENGTH: 981
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-582-861-10841

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Query Match 30.9%; Score 1527.5; DB 6; Length 981;  
Best Local Similarity 37.8%; Pred. No. 5e-138;  
Matches 359; Conservative 168; Mismatches 317; Indels 105; Gaps 29;

Qy	44	TSSGSHCARSRMLRRRAQEEDSTVLID----VSPPEAE-----KRGSYGST---AHASEP	91
		:    :::   :  :         : :	
Db	65	SSSGITNGKTKVFHPVA--KDVNILFDELEAVSSPCKDDDSLHHPGNLTSTSDDASRLEA	122
Qy	92	GGQQAACRAGS-----PAKPRIADFVLVWEEDLKLDRQQDSAARDRTDMHRTWRETFLD	146
		: :       : : : : : :	
Db	123	GGETVPERNKSNGLYFRDGKCRI-DYILVYRK-----SNPQTEK---REVFER	166
Qy	147	NLRAAGLCVDQQDVQDGNTTVHYALLSASWAVLCYYAEDLRLKLPLQE----LPNQASNW	202
		:     :::  : : :            : :::  :    :	
Db	167	NIRAEGLQMEKESSLI-NSDIIFVKLHAPWEVLGRYAEQMNVRMPFRRKIYYLPRRYKFM	225
Qy	203	S-----AGLLAWLGIPNVLL--EVVPDVPP-EYYSRFRVNKLPRFLGSDNQDTFFTST	253
		:    :     :  : :  :   : :  :  :    :	
Db	226	SRIDKQISRFRRWLPKKPMRLDKETLPDLEENDCYTAPFSQQRHHFI-IHNKETFFNNA	284

Qy	254	KRHQILFEILAKTPYGHEKKNLLGIHQLLAEGVLSAAAFPLHDGPFKTPPEGPQAPRLNQR	313
		: :    :        : ::          :  ::	
Db	285	TRSRIVHHILQRIKY-EEGKNKIGLNRLLTNGSYEAAFP LHEGSYRSKNSIRTHGAENHR	343
Qy	314	QVL FQHWARWGKWNKYQPLDHVRRYFGEKVALYFAWLGFYTGWLLPAAVVGTLVFLVGCF	373
		: ::                    :       :          :	
Db	344	HLLYECWASWGVWYKYQPLDLVRRYFGEKIGLYFAWLGWYTGMLFPAAFIGLFVFLYGV	403
Qy	374	LVFSDIPTQELCGSKDSFEMCPLC-LDCPFWLLSSACALAQAGRLFDHGGTVFFSLFMAL	432
		: : :  :     :       :    :   :     :     :	
Db	404	TLDHSQVSKEVCQATDII-MCPVCDKYCPFMRLSDSCVYAKVTHLFDNGATVFFFAVMAV	462
Qy	433	WAVLLLEYWKRKSATLAYRWDCSDYEDTEERPRPQFAAS-APMTAPNPITGEDEPYFPER	491
		:   :   :   :       : :           :    : :	
Db	463	WATVFLEFWKRRRAVIAYDWDLIDWEEEEEEIRPQFEAKYSKKERMNPISGKPEPYQFT	522
Qy	492	SRARRMLAGSVVIVVMVAVVVMCLVSIILYRAIMAIIVSRSGNTLLA-AWA-----SRIA	545
		:  :: :    :   : :  : :  : :        :	
Db	523	DKCSRLIVSASGIFFMICVVIAAVFGIVIVRVTV-----STFAAFKWALIRNNSQVA	575
Qy	546	SLTGSVV--NLVFILILSKIYVSLAHVLTRWEMHRTQTKFEDAFTLKVFIFQFVNFYSSP	603
		:  :      : : :  :  :       :: : :     : :	
Db	576	T-TGTAVCINFCCIIMLLNVLYEKVALLLTNLEQPRTESEWENSFTLKMFLFQFVNLNSST	634
Qy	604	VYIAFFKGRFVGYPGNYHTLFG-VRNEECAAGGCLIELAQELLVIMVGKQVINNMQEVL	662
		:                :  : :          :	
Db	635	FYIAFFLGRFTGHPGAYLRLINRWRL EECHPSGCLIDL CMQMG IIMVLKQTWNNFMELGY	694
Qy	663	PKLKGWWQKFRLRSKKRKAGASAGASQGPWEDDYELVPCE--GLFDEYLEMVLQFGFVTI	720
		: :    :   : :                   :	
Db	695	PLIQNWWR--RKVRQEHGPERKISFPQWEKDYNLQPMNAYGLFDEYLEMILQFGFTTI	751
Qy	721	FVAACPLAPL FALLNNWVEIRLDARKFVCEYRRPVAERAQDIGIWFHILAGLTHLAVISN	780
		:         :  :    :     :      :  : :	
Db	752	FVAAFPLAPLLALLNNIIEIRLDAYKFVTQWRRPLASRAKDIGIWyGILEGIGILSVITN	811
Qy	781	AFLLAFFSSDFLPRAYRW-----TRAHDLRGFLNFTLA-----RAP	816
		:  :  :    : :  :  : :	
Db	812	AFVIAITSDFIPRLVYAYKYGPCAGQGEAGQKCMVGYNASLSVFRISDFENRSEPESDG	871
Qy	817	SSFAAAHNRTCryRAFRDDDGH----YSQTYWNLLAIRLAFVIVFEHVVS VGRLLDLL	871
		: :     :   : : :     :     :    :   :	
Db	872	SEFSGTPLKYCRYRDYRDPHSLVPYGYTLQFHWVLAARLAFIIVFEHLVFCIKHLISYL	931
Qy	872	VPDIPESVEIKVKREYYLAKQALAENEVLFGTNGTKDEQPKGSELSSHW	920
		: : : : : :      : :    :   :   :	
Db	932	IPDLPKDLRDRMRREKYLIQEMMYEAELERLQKERKERKNGKAHHNEW	980

RESULT 8  
US-11-582-861-9875  
; Sequence 9875, Application US/11582861  
; Publication No. US20070099251A1

Query Match 30.5%; Score 1511; DB 6; Length 1046;  
Best Local Similarity 39.7%; Pred. No. 2.2e-136;  
Matches 334; Conservative 156; Mismatches 264; Indels 88; Gaps 25;

[http://es/ScoreAccessWeb/GetItem.action?AppId=10552...124607\\_us-10-552-515-1.rapbm&ItemType=4&startByte=0](http://es/ScoreAccessWeb/GetItem.action?AppId=10552...124607_us-10-552-515-1.rapbm&ItemType=4&startByte=0) (16 of 29)10/10/2008 8:45:58 AM



Qy	557	ILILSKIYVSLAHVLTRWEMHRTQTKFEDAFTLKVFIQFVNIFYSSPVYIAFFKGRFVG	616
		:: :   : ::       ::: ::    : :                  :	
Db	672	IMLLNLAYEKIAYLLTNLEYPRTSEWENSFALKMFLFQFVNLNSSIFYIAFFLGRFVGH	731
Qy	617	PGNYHTLFG-VRNEECAAGGCLIELAQELLVIMVGKQVINNMQEVLPKLGWWQKFRLR	675
		:              :  ::       :     :   ::    : ::	
Db	732	PGKYNKLFDRWRLEECHPSGCLIDLCLQMGVIMFLKQIWNNFMELGYPLIQNWWSRHKI-	790
Qy	676	SKKRKAGASAGASQGPWEDDYELVP--CEGLFDEYLEMVLQFGFVTIFVAACPLAPLFAL	733
		:	
Db	791	----KRGIH-DASIPQWENDWNLQPMNLHGLMDEYLEMVLQFGFTTIFVAAFPLAPLLAL	845
Qy	734	LNNWVEIRLDARKFVCEYRRPVAERAQDIGIWFHILAGLTHLAVISNAFLAFSSDFLPR	793
		:            :    :               :      :    :    : ::	
Db	846	LNNIIEIRLDAYKFVTQWRRPLPARATDIGIWLGLILEGIGILAVITNAFVIAITSYIPR	905
Qy	794	AYYRW-----TRAHDLRGFLNFTLARAP-SSFAAHNRTCRYRAFR-----DDDG	837
		: :  ::  : :   :       :	
Db	906	FVYKEYKYGPCANHVEPSENCLKGYVNNSLSFFDLSELGMGKSGYCRYRDYRGPPWSSKPY	965
Qy	838	HYSQTYWNLLAIRLAFVIVFEHVFSVGRLLDLLVPDIPESVEIKVKREYYLAKQALAEN	897
		::  ::       :     :    : :  :: : : : ::    :: :	
Db	966	EFTLQYWHILAAARLAFIIVFEHLVFGIKSFIAYLIPDVPKGLHDIRREKYLQEMMYEA	1025
Qy	898	EV	899
		:	
Db	1026	EL	1027

RESULT 9

US-11-443-428A-801153  
; Sequence 801153, Application US/11443428A  
; Publication No. US20070083334A1  
; GENERAL INFORMATION:  
; APPLICANT: Mintz, Liat  
; APPLICANT: Xie, Hanqing  
; APPLICANT: Dahari, Dvir  
; APPLICANT: Levanon, Erez  
; APPLICANT: Freilich, Shiri  
; APPLICANT: Beck, Nili  
; APPLICANT: Zhu, Wei-Yong  
; APPLICANT: Wasserman, Alon  
; APPLICANT: Hermesh, Chen  
; APPLICANT: Azar, Idit  
; APPLICANT: Bernstein, Jeanne  
; TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES  
; FILE REFERENCE: 02/23929  
; CURRENT APPLICATION NUMBER: US/11/443,428A  
; CURRENT FILING DATE: 2006-05-31  
; NUMBER OF SEQ ID NOS: 1034312  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 801153  
; LENGTH: 981  
; TYPE: PRT

; ORGANISM: Homo sapiens  
US-11-443-428A-801153

Query Match 30.5%; Score 1508; DB 6; Length 981;  
Best Local Similarity 39.7%; Pred. No. 3.9e-136;  
Matches 334; Conservative 156; Mismatches 264; Indels 88; Gaps 25;

Qy	106	KPRIADFLVWVEEDLKLD	RQQDSAARDRTDMHRTWRETFLDNLRAAGLCVDQQDVQDGNT	165
		::  :	:  :              :::	:
Db	161	KRRI-DYILVYR-----	KTNIPYDKRNTFEKNLRAEGLMLEKEPA-IASP	203
Qy	166	TVHYALLSASWAVLCYYAEDLRLKLP-----	LQELPNQASNWSAGLLA	208
		: : :            :::	:  :	
Db	204	DIMFIKIHIPWDTLCKYAERLNIRMPFRKKCYT	DGRSKSMGRMQTYFRRIKNWMA----	259
Qy	209	WLGIPNVL-LEVVPDV-PPEYYSCRFRVNKLPRFLGSDNQDTFFTSTKRHQILFEILAKT	266	
		: :  :   ::  : :   ::   :  : :  :		
Db	260	--QNPMVLDKSAFPDLEESDCYTGPFSRARIHHFI-INNKDTFFSNATRSRIVYHMLERT	316	
Qy	267	PY--GHEKKNLLGIHQLLAEGVLSAAFPLHDGPFKT----	PPEGPQAPRLNQRVLFQHW	320
		:   : :         :  : :        : : :		
Db	317	KYENGISK---VGIRKLINNGSYIAAFPPEGAYKSSQPIKTHGPQ----	NNRHLLYERW	369
Qy	321	ARWGKWNKYQPLDHVRRYFGEKVALYFAWLGFYTGWLLPAAVVGT	LVFLVGCFLVFS	DIP 380
		:     :      :      :      : :          : :		
Db	370	ARWGMWYKHQPLDLIRLYFGEKIGLYFAWLGWYTGMLIPAAIVGLCVFFYGLFTMNNSQV	429	
Qy	381	TQELCGSKDSFEMCPLC-LDCPFWLLSSACALAQAGRLFDHGGTVFFSLFMALWAVLLE	439	
		:  :  : :        :   : :   :   :     : : :    :		
Db	430	SQEICKATEVF-MCPLCDKNCSLQRLNDSCIYAKVTYLF	DNGGTVFFAIFMAIWATVFLE	488
Qy	440	YWKRKSATLAYRWDCSDYEDTEERPRPQFAAS-APMTAPNPITGEDEPYFPERSRARRML	498	
		:  : :        :  :                 :   :   :  :		
Db	489	FWKRRRSILTYTWDLIEWEEEEETLRPQFEAKYYKMEIVNPITGKPEPHQPSSDKVTRLL	548	
Qy	499	AGSVVIVVMVAVVVMCLVSIILYR-AIMAIVVSRSGNTLLAAWASRIASLTGSV-VNLVF	556	
		:: : : ::   :    :   :  :  :  :		
Db	549	VSVSGIFFMISLVITAVFGVVVYRLVMEQFASFKNWFIKQYW--QFATSAAAVCINFII	606	
Qy	557	ILILSKIYVSLAHVLTRWEMHRTQTKFEDAFTLKVFIFQFVN	FYSSPVYIAFFKGRFVGY	616
		:: :   : :       ::: :   : :                 :		
Db	607	IMLLNLAYEKIAYLLTNLEYPRTSEWENSFALKMFLFQFVNLN	SSIFYIAFFLGRFVGH	666
Qy	617	PGNYHTLFG-VRNEECAAGGCLIELAQELLVIMVGKQVINNMQEV	LIPKLKGWWQKFLR	675
		:             :  ::     :   :   :  :  :		
Db	667	PGKYNKLFDRWRLEECHPSGCLIDLCLQMGVIMFLKQIWN	NFMELGYPLIQNWWSRHKI-	725
Qy	676	SKKRKAGASAGASQGPWEDDYELVP--CEGLFDEYLEMVLQFGF	VTIFVAACPLAPL	FAL 733
		: :		
Db	726	----KRGIH-DASIPQWENDWNLQPMNLHGLMDEYLEMVLQFGF	TTIFVAAFPLAPLLAL	780
Qy	734	LNNWVEIRLDARKEFVCEYRRPVAERAQDIGIWFHILAGLTHL	AVISNAFLLA	FSSDFLPR 793
		:        :   :              :    : : :  : :		
Db	781	LNNIEIRLDAYKFVTQWRRPLPARATDIGIWLGILEGIGILAVIT	NAFVIAITS	SDYIPR 840

Qy 794 AYYRW-----TRAHDLRGFLNFTLARAP-SSFAAAHNRTCryRAFR-----DDDG 837  
| : : |:|:| :|: | : ||| :|  
Db 841 FVYKYKYGPCANHVEPSENCLKGYVNNSLSFFDLSELGMGKSGYCRYRDIRGPPWSSKPY 900  
  
Qy 838 HYSQTYWNLLAIRLAFVIVFEHVFSVGRLLDLLVPDIPESVEIKVKREYYLAKQALAEN 897  
: : ||:| | |||:| |||:| : : |:|:|: : : :| | : : |  
Db 901 EFTLQYWHILAAARLAFIIVFEHLVFGIKSFIAYLIPDVPKGLHDIRRREKYLQEMMYEA 960  
  
Qy 898 EV 899  
|:  
Db 961 EL 962

RESULT 10

US-11-177-894-7  
; Sequence 7, Application US/11177894  
; Publication No. US20060040292A1  
; GENERAL INFORMATION:  
; APPLICANT: West, et al.  
; TITLE OF INVENTION: Tumor Markers and Uses Thereof  
; FILE REFERENCE: 2002850-0048  
; CURRENT APPLICATION NUMBER: US/11/177,894  
; CURRENT FILING DATE: 2005-07-08  
; NUMBER OF SEQ ID NOS: 29  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 7  
; LENGTH: 960  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Transmembrane protein  
US-11-177-894-7

Query Match 30.1%; Score 1488; DB 6; Length 960;  
Best Local Similarity 37.6%; Pred. No. 3.4e-134;  
Matches 363; Conservative 160; Mismatches 307; Indels 136; Gaps 28;

Qy 26 GLYCRDQAHAERWAMT--SETSSGSHCARSRMLRRRAQEEDSTVLIDVSPPEAEKRGSYG 83  
||| || : : : || :| | || | |:  
Db 52 GLYFRDGRRKVDYILVYHHKRPSPG-----NRTLVRVRVQHSDTP-----SGA 92  
  
Qy 84 STAHASEPGGQQAACRAGSPAKPRIADFLVWEEEDLKLDRQQDSAARDRTDMHRTWRET 143  
: | : |: ||| | :| :| | ||  
Db 93 RSVKQDHPLPGKGASLDAGSGEPP-----MDYHEDD-----KRFRREE 130  
  
Qy 144 FLDNLRAAGLCVDQQDVQDGNTTVH--YALLSASWAVLCYYAEDLRLKLPLQELPNQAS 200  
: || ||| : : :| :| : : | | || | | :|:|:| : : :  
Db 131 YEGNLLLEAGLELE----RDEDTKIHGVGVFKIHAPWNVLCREAEFLKLKMPTKKMYH--I 184  
  
Qy 201 NWSAGLLAWLGIPNVLLLEVVPDVPPEYYSCR-----FRVKNLPRFLGSDNQDTFF 250  
| : ||| | :|| : : :| : | | | | :|:|  
Db 185 NETRGLLK--KINSVLQKITDPIQPKVAEHRPQTMKRLSYFPSREKQHLFDLSD-KDSFF 241

Qy	251	TSTKRHQILFEILAKTPYGHEKKNLLGIHQLLAEGVLSAAFPLHDGPFKTPPEGPQAPRL	310
		::    :    : :          :  :      : :	
Db	242	DSKTRSTIVYEILKRTTCTKAKYS-MGITSLLANGVYAAAYPLHDGDY-----NGENVEF	295
Qy	311	NQRQVLFQHWARWGKWNKYQPLDHVRRYFGEKVALYFAWLGFYTGWLLPAAVVGTLVFLV	370
		:: ::    :  :     :    :    :           :: ::   :	
Db	296	NDRKLLYEEWARYGVFYKYQPIDLVRKYFGEKIGLYFAWLGVYTQMLIPASIVGIIIVFLY	355
Qy	371	GCFLVFSDIPTQELCGSKDSFEMCPLC-LDCPFWLLSSACALAQAGRLFDHGGTVFFSLF	429
		: :  :  :  : :        :  :      :     :     :	
Db	356	GCATMDENIPSMEMCDQRHNITMCPLCDKTCSYWKMSACATARASHLFDNPATVFFSVF	415
Qy	430	MALWAVLLLEYWKRKSATLAYRWDCSDYEDTEE----RPRPQFAA-----SAPMTAPNPI	480
		::           : :        :    :	
Db	416	MALWAATFMEHWKRKQMRNLNYRWDLTGFEEEEEAVKDHPRAEYEARVLEKSLKKESRNKE	475
Qy	481	TGEDEPYFPERSRARRMLAGSVVIVVMVAVVMCLVSIILYRAIMAIIVSRSGNTLLAAW	540
		:       : :  : : :     : : : : :	
Db	476	T--DKVKLTWRDRFPAYLTNLVSIIFMIAVTFAIVLGVIIYRISMAAALAMNSSPSVRSN	533
Qy	541	ASRIASLTGSVVNLVFILILSKIYVSLAHVLTRWEMHRTQTKFEDAFTLKVFIQFVNFI	600
		:   :     :  :  :    :  : : :   :    : :	
Db	534	IRVTVTATAVIINLVIIILLDEVYGCJARWLTKIEVPKTEKSFEERLIFKAFLCLKFVNSY	593
Qy	601	SSPVYIAFFKGRFVGYPGNYHTLF-GVRNEECAAGGCLIELAQELLVIMVGKQVI-NNMQ	658
		:  ::          :  :           :    : :  : :    :	
Db	594	TPIFYVAFFKGRFVGRPGDYVYIFRSFRMEECAPGGCLMELCIQLSIIMLGKQLIQNNLF	653
Qy	659	EVLIPKLGWWQKFRLRSKKRKAGASAGASQGPWEDDYELVPCEGLFDEYLEMVLQFGFV	718
		:   :  : : : : : :              : : :	
Db	654	EIGIPKMKKLIRYLKQKQSPPDHEECVKKRQRYEVDYNLEPFAGLTPEYMEMIIQFGFV	713
Qy	719	TIFVAACPLAPLFAALLNNWVEIRLDARKFVCEYRRPVAERAQDIGIWFHILAGLTHLAVI	778
		:   :            :   :             :   : :   :	
Db	714	TLFVASFPLAPLFAALLNNIIEIRLDAKKFVTELRRPVAVRAKDIGIWYNILRGIGKLAVI	773
Qy	779	SNAFLLAFSSDFLPRA--YYRWTRAHDLRGFLNFTLARAPSSF-----AAAHN-----	824
		:: : : :    ::: :  :	
Db	774	INAFVISFTSDFIPRLVLYLYMSKNGTMHGFVNHTL----SSFNVSDFQNGTAPNDPLDL	829
Qy	825	----RTCRYRAFRD---DDGHY--SQTYWNLLAIRLAFVIVFEHVVFSGRLLDLLVPDI	875
		:    :  :  :    : :  :         : :  : :  :	
Db	830	GYESQICRYKDYREPPWSENKYDISKDFWAVLAARLAFVIVFQNLVFMMSDFVDWVIPDI	889
Qy	876	PESVEIKVKREYYLA-----KQALAENEVLFGTNGTKDEQP-----KG	913
		: : : :	
Db	890	PKDISQQIHKEKVLMMVELFMREEQDKQQLL--ETWMEKERQKDEPPCNHHNTKACPDSLG	947
Qy	914	SELSSH	919
Db	948	SPAPSH	953

```
; Sequence 11, Application US/11177894
; Publication No. US20060040292A1
; GENERAL INFORMATION:
;   APPLICANT: West, et al.
;   TITLE OF INVENTION: Tumor Markers and Uses Thereof
;   FILE REFERENCE: 2002850-0048
;   CURRENT APPLICATION NUMBER: US/11/177,894
;   CURRENT FILING DATE: 2005-07-08
;   NUMBER OF SEQ ID NOS: 29
;   SOFTWARE: PatentIn version 3.2
; SEQ ID NO 11
;   LENGTH: 840
;   TYPE: PRT
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: Homo sapiens
```

US-11-177-894-11

Query Match 29.9%; Score 1479.5; DB 6; Length 840;  
Best Local Similarity 40.0%; Pred. No. 1.8e-133;  
Matches 340; Conservative 152; Mismatches 270; Indels 89; Gaps 22;

Qy 135 DMHRTWRETFLDNLRAAGLCVDQQDVQDGNTTVH---YALLSASWAVLCYYAEDLRLKLP 191  
| | || : || ||| :: :| :| :| : : | | || | || :||:|  
Db 6 DDKRFRREEYEGNLLLEAGLELE----RDEDTKIHGVGFKIHAPWNVLCREAEFLKLKMP 61

Qy 192 LQELPNQASNWSAGLLAWLGIPNVLLEVPDVPPEYYSCR-----FRVNKLPRFL 241  
::: | : || | : || :: : | : | |

Db 62 TKKMYH--INETRGLLK--KINSVLQKITDPIQPKVAEHRPQTMKRLSYPFSSREKQHLFD 117

Qy 242 GSDNQDTFFTSTKRHQILFEILAKTPYGHEKKNLLGIHQLLAEGVLSAAFPLHDGPFKTP 301  
 || :||:| | | | ::||| :| | : :|| ||| || :||:||||| :  
 Db 118 LSD-KDSFFDSKTRSTIVYEILKRTTCTKAKYS-MGITSLLANGVYAAAYPLHDGDY--- 172

Qy 302 PEGPQAPRLNQRQVLFQHWARWGKWNKYQPLDHVRRYFGEKVALYFAWLGFYTGWLLPAA 361  
: | |::|:: |||:| : ||||:| ||:||||: ||||| | | |::|:  
Db 173 --NGENVEFNDRLKLLYEEWARYGVFYKYQPIDLVRKYFGEKIGLYFAWLGVYTQMLIPAS 230

Qy 362 VVGTLVFLVGCFLVFSDIPTQELCGSKDSFEMCPLC-LDCPFWLLSSACALAQAGRLFDH 420  
:|| :||| || : :||: |:| : : |||| | :| :|||| |:| |||:

Db 231 IVGIIVFLYGCATMDENIPSMEMCDQRHNITMCPCLCDKTC SYWKMS SACATARASHLFDN 290

Qy 421 GGTVFFSLFMALWAVLLLEYWKRKSATLAYRWDCSDYEDTEERPRPQFAA-----SAPMT 475  
 |||||:||||| :||:|||| | |||| : :||: || :: | |  
 Db 291 PATVFFSVFMALWAATFMEHWKRKQMRLNRYRWDLTGFEEEDHPRAEYEARVLEKSLKKE 350

Qy 476 APNPITGEDEPYFPERSRARRMLAGSVVIVVMVAVVVMCLVSIILYRAIMAIVVSRSGNT 535  
: | | |: | | | |: |:| | :: |:| | || :: : :  
Db 351 SRNKET--DKVKLTWRDRFPAYLTNLVSIIFMIAVTFAIVLGVIIYRISMAAALAMNSSP 408

Qy 536 LLAAWASRIASLTGSVVNLVFIILSKIYVSLAHVLTRWEMHRTQTKFEDAFTLKVFIFQ 595  
: : : | ::||| |::| ::| :| ||: |: ::| ||: | |: :  
Db 409 SVRSNIRVTVTATAVIINLVVVIILLDEVYGCJARWLTKIEVPKTEKSFEERLIFKAFLK 468

Qy	596	FVNFYSSPVYIAFFKGRFVGYPGNYHTLF-GVRNEECAAGGCLIELAQELLVIMVGKQVI	654
		:  :          :  :           :    :   :   :	
Db	469	FVNSYTPIFYVAFFKGRFVGRPGDYVYIFRSFRMEECAPGGCLMELCIQLSIIMLGKQLI	528
Qy	655	-NNMQEVLIPKLKGWWQKFRRLRSKKRKAGASAGASQGPWEDDYELVPCEGLFDEYLEMVL	713
		:  :    :  : : : : : :             :   :	
Db	529	QNNLFEIGIPKMKKLIRYLKLKQQSPPDHEECVKRKQRYEVDYNLEPFAGLTPEYMEMII	588
Qy	714	QFGFVTIFVAACPLAPLFAALLNNWVEIRLDARKFVCEYRRPVAERAQDIGIWFHILAGLT	773
		:   :            :     :           :   :   :    :	
Db	589	QFGFVTILFVASFPLAPLFAALLNNIIEIRLDAKKFVTELRRPVAVRAKDIGIWNILRGIG	648
Qy	774	HLAVISNAFLLAFFSSDFLPRA--YYRWTRAHDLRGFLNFTLARAPSSF-----AAAHN	824
		:   :   :   :    : : : :  :	
Db	649	KLAVIIDAFVISFTSDFIPRLVLYLYMYSKNGTMHGFVNHTL----SSFNVSDFQNGTAPN	704
Qy	825	-----RTCRYRAFRD---DDGHY--SQTYWNLLAIRLAFVIVFEHVVSFVGRLLDL	870
		:    :  : : :    :  :   :       :   :  : :	
Db	705	DPLDLGYEVQICRYKDYREPPWSENKYDISKDFWAVLAARLAFVIVFQNLVMFMSDFVDW	764
Qy	871	LVPDIPESVEIKVKREYYLA-----KQALAENEVLFGTNGTKDEQP-----	911
		:   :   : : : :	
Db	765	VIPDIPKDISQQIHKEKVLMMVELFMREEQDKQQLL--ETCMEKERQKDEPPCNHHNTKAC	822
Qy	912	---KGSELSSH	919
Db	823	PDSLGGSPAPSH	833

RESULT 12  
US-11-443-428A-774192  
; Sequence 774192, Application US/11443428A  
; Publication No. US20070083334A1  
; GENERAL INFORMATION:  
; APPLICANT: Mintz, Liat  
; APPLICANT: Xie, Hanqing  
; APPLICANT: Dahari, Dvir  
; APPLICANT: Levanon, Erez  
; APPLICANT: Freilich, Shiri  
; APPLICANT: Beck, Nili  
; APPLICANT: Zhu, Wei-Yong  
; APPLICANT: Wasserman, Alon  
; APPLICANT: Hermesh, Chen  
; APPLICANT: Azar, Idit  
; APPLICANT: Bernstein, Jeanne  
; TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES  
; FILE REFERENCE: 02/23929  
; CURRENT APPLICATION NUMBER: US/11/443,428A  
; CURRENT FILING DATE: 2006-05-31  
; NUMBER OF SEQ ID NOS: 1034312  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 774192  
; LENGTH: 999

; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-443-428A-774192

Query Match 29.6%; Score 1464; DB 6; Length 999;  
Best Local Similarity 37.4%; Pred. No. 7.7e-132;  
Matches 344; Conservative 167; Mismatches 284; Indels 124; Gaps 27;

Qy	80	GSYGSTAHASEPGGQQAACRAGSPAKPRIADFLVWVEEDLKLDROQDSAARDRTDMHRT	139
		::    :   :	
Db	125	GETGKEPHAGGPG-----DIELG-PLDALEEEERKEQ---	154
Qy	140	WRETFLDNLRAAGLCVDQQDVQDGNTTVHYALLSASWAVLCYYAEDLRLKLPLQELPNQ-	198
		: ::  : : : :            ::   : : :	
Db	155	-REEFEHNLMEAGLEL-EKDLENKSQGSIFVRIHAPWQVLAREAEFLKIKVPTKKEMYEI	212
Qy	199	-----ASNWSAGLLAWLGIPNVLLEVVPDPPEYYSCRFRVNKLP-----RFLGSDNQ	246
		:     : :       : : : :   :	
Db	213	KAGGSIAKKFSAAAL-----QKLSSHLQPRV-PEHSNNKMKNLSYPFSREKMYLYNIQEK	265
Qy	247	DTFFTSTKRHQILFEILAKTPYGHEKKNLLGIHQLLAEGVLSAAFPPLHDGPFKTPPEGPQ	306
		:   :       :    :  :  :  :   :     : :  :	
Db	266	DTFFDNATRSRIVHEILKRTACS-RANNTMGINSLIANNIYEAAAYPLHDGEYDSPEDD--	322
Qy	307	APRLNQRQVLFQHWARWGKWNKYQPLDHVRRYFGEKVALYFAWLGFYTGWLLPAAVVGTL	366
		:   ::      :  :  ::   : :    :          : : :: :  :	
Db	323	---MNDRKLLYQEWARYGVFYKFQPIDLIRKYFGEKIGLYFAWLGLYTSFLIPSSVIGVI	379
Qy	367	VFLVGCFLVFSDIPTQELCGSKDSFEMCPLC-LDCPFWLLSSACALAQAGRLFDHGGTVF	425
		:    ::  : :::         :              :	
Db	380	VFLYGCATIEEDIPSREMCDQQNAFTMCPLCDKSCDYWNLSSACGTAQASHLFDNPATVF	439
Qy	426	FSLFMALWAVLLLEYWKRKSATLAYRWDCSDYEDTEER---PRPQFAA-----	470
		:      :               :   :       ::	
Db	440	FSIFMALWATMFLENWKRLQMRLGYFWDLTGIEEEEEERAQEHSRPEYETKVREKMLKESN	499
Qy	471	-SAPMTAPNPIT---GEDEPYFPERSRARRMLAGSVVIVVMVAVVVMCLVSIILYRAIM	525
		:   :       :  ::  : : : :	
Db	500	QSAVQKLETNTTECGDEDEDKLTWKDRFPGYLMNFASILFMIALTFSIVFGVIVYRITT	559
Qy	526	AIVVSRSGNTLLAAWASRI---ASLTGSVNLVFILILSKIYVSLAHVLTRWEMHRTQTK	582
		:        : :   :         :   :    :   :  :	
Db	560	AAALS-----LNKATRSNVRVTVTATAVIINLVILILDEIYGAVAKWLTKIEVPKTEQT	614
Qy	583	FEDAFTLKVFIFQFVNFYSSPVYIAFFKGRFVGYPGNYHTLF-GVRNEECAAGGCLIELA	641
		:      : :        :          :  :              :	
Db	615	FEERLILKAFLLKFVNAYSPIFYVAFFKGRFVGRPGSYVYVFDGYRMEECAPGGCLMELC	674
Qy	642	QELLVIMVGKQVI-NNMQEVLIPKLKGWWQKFRLRSKKRKAGASAGA-SQGP--WEDDYE	697
		:  :  : ::    :   : :    :    : :   :     :     :	
Db	675	IQLSIIMLGKQLIQNNIFEIGVPKLK---KLFRKLKDETEAGETDSAHSKHPEQWDLDYS	731
Qy	698	LVPCEGLFDEYLEMVLQFGFVTIFVAAACPLAPLFAALLNNWVEIRLDARKFVCEYRRPVAE	757
		: : :     : ::     :      : :    :	

Db	732	LEPYTGLTPEYMEMIIQFGFVTLFVASFPLAPVFALLNNVIEVRLDAKKFVTELRRPDAV	791
Qy	758	RAQDIGIWFHILAGLTHLAVISNAFLFSSDFLPRAYRWTRAHD--LRGFLNFTLA--	813
		:        :  :      ::  :  :    :: :  :     :    :	
Db	792	RTKDIGIWFIDILSGIGKFSVISNAFVIAITSDFIPRLVYQYSYSHNGTLHGFEVNHTLSFF	851
Qy	814	-----RAPSSFAAAHNRTCRYRAFRD-----DDGHYSQTYWNLLAIRLAFVIVFEH	859
		: :  :   : :  : : :  :    :  :      : ::	
Db	852	NVSQLKEGTQPENSQFDQEVQFCRFKDYREPPWAPNPYEFQYWFILSARLAFVIIFQN	911
Qy	860	VVFSVGRLLDLLVPDIPESVEIKVKRE-----YYLAKQALAENEVLFGTNGTKDEQPKG	913
		:  :  :  ::    : :: :  ::  :  :    :	
Db	912	LVMFLSVLVDWMIPDIPTDISDQIKKEKSLLVDFFLKE----EHEKLKLMDEPALRSPGG	967
Qy	914	SELSSHWPFTVPKA-SQL	931
		:   :	
Db	968	GDRSRRAASSAPSGSQL	986

RESULT 13

US-11-097-143-15228  
; Sequence 15228, Application US/11097143  
; Publication No. US20050208558A1  
; GENERAL INFORMATION:  
; APPLICANT: Venter, J. Craig  
; APPLICANT: et al.  
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID  
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE  
; TITLE OF INVENTION: DROSOPHILA GENES.  
; FILE REFERENCE: CL000728  
; CURRENT APPLICATION NUMBER: US/11/097,143  
; CURRENT FILING DATE: 2005-04-04  
; PRIOR APPLICATION NUMBER: 60/157,832  
; PRIOR FILING DATE: 1999-10-05  
; PRIOR APPLICATION NUMBER: 60/160,191  
; PRIOR FILING DATE: 1999-10-19  
; PRIOR APPLICATION NUMBER: 60/161,932  
; PRIOR FILING DATE: 1999-10-28  
; PRIOR APPLICATION NUMBER: 60/164,769  
; PRIOR FILING DATE: 1999-11-12  
; PRIOR APPLICATION NUMBER: 60/173,383  
; PRIOR FILING DATE: 1999-12-28  
; PRIOR APPLICATION NUMBER: 60/175,693  
; PRIOR FILING DATE: 2000-01-12  
; PRIOR APPLICATION NUMBER: 60/184,831  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: 60/191,637  
; PRIOR FILING DATE: 2000-03-23  
; NUMBER OF SEQ ID NOS: 43008  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 15228  
; LENGTH: 1219  
; TYPE: PRT  
; ORGANISM: DROSOPHILA



US-11-097-143-15228

Query Match 29.2%; Score 1445; DB 6; Length 1219;  
 Best Local Similarity 35.6%; Pred. No. 7.3e-130;  
 Matches 342; Conservative 165; Mismatches 332; Indels 122; Gaps 27;

```

Qy      35 AERWAMTSETSSGSHCARSRML-----RRRAQEEDSTVLIDVSPPEAEKRGSY 82
      |:|  : |  ||  | :|  | :|  : | :|  |||
Db      249 ADRVNQSYEVMESSEH---SNVLPDQFGYRQLIPTERKASDTASSV-----SGSY 294

Qy      83 GSTAHASEP---GGQQAACRAGSPAKP-----RIADFVLVW-EEDLKLDRQ 125
      :  ||:  ||:  |  :  |  |  ||  |  |||  :  :
Db      295 YGSRKASKSNSLGGESGDERRVSKQDREGLDPESLMFRDGRRKVDMVLAWEEEDLGVMT 354

Qy     126 QDSAARDRTDMHRTWRETFLDNLRAAGLCVDQQD-VQDGNTTVHYALLSASWAVLCYYAE 184
      ::  ||  |  ::::||  ||  | :  :|  |  |  :  :  |  :  ||
Db     355 AEAKRRDN-----RRSFMENLIKEGLEVELEDKSQSFNEKTFFLKIHLPWRLLETRLAE 407

Qy     185 DLRLKLP-----LQELPNQASNWSAGLLAWLGIPNVLLLEVVPDVPP 225
      :  ||||  | :  :  |  |  :  :  |||
Db     408 VMNLKLPVKRFITISVKPSWDEENVVLRLNMQYWKDVWQR-LTKKIQLDQTILLE----GET 462

Qy     226 EYYSCRFRVNKLPRFLGSDNQDTFFTSTKRHQILFEILAKTPYGHEKKNLLGIHQLLAEG 285
      :  :  |  :|:  |  :  |  |||  :|  ::  ::|  :||:  :  :  ||  :|:  :|
Db     463 TFKAATANGNPEEQFIVKD-RATAFTSAQRSLMVMQVLIRTPFDESQRS--GIRRLMNDG 519

Qy     286 VLSAAFPLHDGPFKTPPEGPQAPRLN-QRQVLFQHWARWGKWNKYQPLDHVRRYFGEKVA 344
      ||||:|  :  :  |  :  ::  |::||  ||  :|  |  |||  ||:||||:|:|
Db     520 TYLGCFLHEGRY----DRPHSSGISLDRRVLYQTWAHPSQWYKKQPLCLVRKYFGDKIA 575

Qy     345 LYFAWLGFYTGWLLPAAVVGTLLVFLVGCFLVFSD--IPTQELCG--SKDSFEMCPLC-LD 399
      |||  |||||  |:  |||||  |:  |  :  |:  |::||  :  :|||
Db     576 LYFCWLGFYTEMLVYPVVGTLCFIYGLATLESEDNTPSKEICNEYGTGNITLCPLCDKA 635

Qy     400 CPFWLLSSACALAQAGRLFDHGGTVFFSLFMALWAVLLLEYWKRKSATLAYRWDCSDYED 459
      |  :  ||  :|  ::  |||:  ||||::||:  ||  ||  ||||  :  |  :  ||  :  |
Db     636 CSYQRLSESCFLSRLTYLFDNPSTVFFAIFMSFWATTFLLELWKRKQSVLVWEWDLHNV-D 694

Qy     460 TEERPRPQFAASAPMTAPNPITGEDEPYFPERSRARRMLAGSVVIVVMVAVVVMCLVSII 519
      :|  ||:|  :|  ||:|  |  |||  :|:  |  :  :  :|::||:  :  :  |
Db     695 MDEENRPEFETNATTFRMNPVTREKEPYMSTWNRSIRFVITGSAVLFMISVVLSAVLGTI 754

Qy     520 LYRAIMAIVVSRSNTLLAAWASRIASLTGSSVNLVFIILISKIYVSLAHVLTRWEMHRT 579
      |||  :  |:  |  :  |  |:|  :::||||  |:|::||  :|  ||  |  ||
Db     755 LYRITLVSVIYGGGGFFVKEHAKLFTSVTAALINLVVIMILTRIYHRMAIKLTNLENPRT 814

Qy     580 QTKFEDAFTLKVFIFQFVNFYSSPVYIAFFKGRFVGYPGNYHT----LFGVRNEECAAGG 635
      |::||::|  |:|  |::|:||||  :|||||||  |||:  |  ::|:  |  |
Db     815 HTEYEDSYTFKIFFFEFMNFYSSLIYIAFFKGRFFDYPGDDQARKSEFFRLKNDICDPAG 874

Qy     636 CLIELAQELLVIMVGKQVINNMQEVLPKLGWWQKFRLRSKKRKAGASAGASQGPWEDD 695
      ||  ||  :|  :|||||  ||  |  ||  ||:  :  |  :|  ||  |
Db     875 CLSELCIQLAIIMVGKQCWNMFMEYLFPKFWNWWR----QRKHKQATKDESHLHMAWEQD 930

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Qy	696	YELV-PCE-GLFDEYLEMVLQFGFVTIFVAACPLAPLFALLNNWVEIRLDARKFVCEYRR	753
		:        : : : :                  :	
Db	931	YHMQDPGRLLALFDEYLEMILQYGFVTLFVAAFPLAPLFALLNNVAEIRLDAYKMVTQARR	990
Qy	754	PVAERAQDIGIWFHILAGLTHLAVISNAFLLAFSSDFLPRAYYR--WTRAHDLRGFLNFT	811
		:    :     :     :   :    : : : :    : ::      : : :	
Db	991	PLAERVEDIGAWYGILRIITYTAVVSNAFVIAYTSDFIPRMVYKFVYSEHTLAGYIEHS	1050
Qy	812	LA-----RAPSSFAAAHNRTCryRAFRDDDGHY-----SQTyWnLLAIRLAFVIVF	857
		: : :   :  :  :     :        :	
Db	1051	LSIFNTSDYKEEWGASVSEKDPDTCQYRGYRNGPKDYEPYGLSPHYWHVFAARLAFVVVF	1110
Qy	858	EHVVFsvGRLldLLVPDIPESVEIKVKREYYLAKQALAENEVLFGTNGTKDEQPKGSELS	917
		: :: :  :   : ::     :  : :      ::	
Db	1111	EHVVFVITGIMQFIIPDVPSEVKTQMQREQLLAKEAKYQ-----HGikRAQGDSQDIM	1163
Qy	918	S 918	
Db	1164	S 1164	

RESULT 14  
US-11-443-428A-739452  
; Sequence 739452, Application US/11443428A  
; Publication No. US20070083334A1  
; GENERAL INFORMATION:  
; APPLICANT: Mintz, Liat  
; APPLICANT: Xie, Hanqing  
; APPLICANT: Dahari, Dvir  
; APPLICANT: Levanon, Erez  
; APPLICANT: Freilich, Shiri  
; APPLICANT: Beck, Nili  
; APPLICANT: Zhu, Wei-Yong  
; APPLICANT: Wasserman, Alon  
; APPLICANT: Hermesh, Chen  
; APPLICANT: Azar, Idit  
; APPLICANT: Bernstein, Jeanne  
; TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES  
; FILE REFERENCE: 02/23929  
; CURRENT APPLICATION NUMBER: US/11/443,428A  
; CURRENT FILING DATE: 2006-05-31  
; NUMBER OF SEQ ID NOS: 1034312  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 739452  
; LENGTH: 800  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-443-428A-739452

Query Match 28.6%; Score 1417; DB 6; Length 800;  
Best Local Similarity 40.3%; Pred. No. 2e-127;  
Matches 326; Conservative 142; Mismatches 252; Indels 88; Gaps 22;

Qy	179	LCYYAEDLRLKLPLQELPNQASNWSAGLLAWLGIPNVLLLEVVPDVPPEYYSCR-----	231
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Db	7	LC--ARVLKCLKMPTKKMYH--INETRGLLK--KINSVLQKITDPIQPKVAEHRPQTMKRL	60
Qy	232	---FRVKNLPRFLGSDNQDTFFTSTKRHQILFEILAKTPYGHEKKNLLGIHQLLAEGVLS	288
Db	61	SYFPSREKQHLFDLSD-KDSFFDSKTRSTIVYEILKRTTCTKAKYS-MGITSLLANGVYA	118
Qy	289	AAFPLHDGPFKTPPEGPQAPRLNQROVLFGHVARWGKWNKYQPLDHVRRYFGEKVALYFA	348
Db	119	AAYPLHDGDY-----NGENVEFNDRLKLLYEWEARYGVFYKYQPIDLVRKYFGEKIGLYFA	173
Qy	349	WLGfYtGWLLPAAVVGTLVFLVGCFLVFSDIPTQELCGSKDSFEMCPLC-LDCPFWLLSS	407
Db	174	WLGvYtQMLIPASIVGIIVFLYGCATMDENIPSMEMCDQRHNITMCPLCDKTCsyWKMSS	233
Qy	408	ACALAQAGRLFDHGGTVFFSLFMALWAVLLLEYWKRKSATLAYRWDCSDYEDTEE---R	463
Db	234	ACATARASHLFDNPATVFFSVFMALWAATFMEHWKRKQMRLNyrWDLTGfEEEEEEAVKDH	293
Qy	464	PRPQFAA-----SAPMTAPNPITGEDEPYFPERSRARRMLAGSVVIVVMVAVVVMCLVSI	518
Db	294	PRAEYEARVLEKSLKKESRNKET--DKVKLTWRDRFPAYLTNLVSIIFMIAVTFaIVLGV	351
Qy	519	ILYRAIMAIVVSRSGNTLLAAWASRIASLTGSVNNLVFILILSKIYVSLAHVLTRWEMHR	578
Db	352	IIYRISMAAALAMNSSPSVRSNIRVTVTATAVIINLVVIILLDEVYGCiARWLTKIEVPK	411
Qy	579	TQTKFEDAFTLKVFIFQFVNfYSSPVYIAFFKGRFVGYPGNYHTLF-GVRNEECAAGGCL	637
Db	412	TEKSFEERLIFKAFLKfVNSYtPIFYVAFFKGRFVGRPGDYVYIFRsfRMEECAPGGCL	471
Qy	638	IELAQELLVIMVGKQVI-NNMQEVLIpKLKGWWQKfRLRSKkrKAGASAGASQGPWEDDY	696
Db	472	MELCIQLSIIMLGKQLIqNNLFEIGIPKMKKLiRYLKLKQQSPPDHEECVkrKQRYEVDY	531
Qy	697	ELVPCEGLFDEYLEMVlQFGFvTIFVAACPLAPLFAllNNWVEIRLDARKfVCEYRRPVA	756
Db	532	NLEPFAGLTPEYMEMIIQFGFvTLFVASfPLAPLFAllNNIIEIRLDAKKfVTELRRPVA	591
Qy	757	ERAQDIGIWfHILAGLTHLAVISNAfLLAFSSDFLPRA--YyRWTRAHDLRGfLNFTLAR	814
Db	592	VRAKDIGIWYNILRGIGKLAVIINAFVISfTSDFIPRLVYLYMYSKNGTMHGfVNHTL--	649
Qy	815	APSSF-----AAAHN-----RTCRYRAFRD---DDGHY--SQTyWNLLAIRLAF	853
Db	650	--SSFNVSDfQNGTAPNDPLDLGYEVQICRYKDYREPPWSENKYDISKDFWAVLAARLAF	707
Qy	854	VIVFEHVfVSVGRLLDLLVPDIPESVEIKVKREYYLA-----KQALAENEVLFGT	903
Db	708	VIVfQNLVMfMSDFVDWVIPDIPKDISQqIHKEKVLmVELFMREEQDKQQLL--ETWMEK	765
Qy	904	NGTKDEQP-----KGSELSSH	919
Db	766	ERQKDEPPCnHHNTKACPDSLgSPAPSH	793

RESULT 15

US-11-443-428A-739454  
; Sequence 739454, Application US/11443428A  
; Publication No. US20070083334A1  
; GENERAL INFORMATION:  
; APPLICANT: Mintz, Liat  
; APPLICANT: Xie, Hanqing  
; APPLICANT: Dahari, Dvir  
; APPLICANT: Levanon, Erez  
; APPLICANT: Freilich, Shiri  
; APPLICANT: Beck, Nili  
; APPLICANT: Zhu, Wei-Yong  
; APPLICANT: Wasserman, Alon  
; APPLICANT: Hermesh, Chen  
; APPLICANT: Azar, Idit  
; APPLICANT: Bernstein, Jeanne  
; TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES  
; FILE REFERENCE: 02/23929  
; CURRENT APPLICATION NUMBER: US/11/443,428A  
; CURRENT FILING DATE: 2006-05-31  
; NUMBER OF SEQ ID NOS: 1034312  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 739454  
; LENGTH: 800  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-443-428A-739454

Query Match	28.6%;	Score 1417;	DB 6;	Length 800;
Best Local Similarity	40.3%;	Pred. No. 2e-127;		
Matches	326;	Conservative 142;	Mismatches 252;	Indels 88; Gaps 22;
Qy	179	LCYYAEDLRLKLPQLQELPNQASNWSAGLLAWLGIPNVLLVVPDVPPEYYSCR-----	231	
		: :  :: :   :        :   :: :   :		
Db	7	LC--ARVLKCLKMPTKKMYH--INETRGLLK--KINSVLQKITDPIQPKVAEHRPQTMKRL	60	
Qy	232	---FRVKNKLPRFLGSDNQDTFFTSTKRHQILFEILAKTPYGHEKKNLLGIHQLLAEGVLS	288	
		: :        : :    :  : :        :		
Db	61	SYPFSSREKQHLFDLSD-KDSFFDSKTRSTIVYEILKRTTCTKAKYS-MGITSLLANGVYA	118	
Qy	289	AAFPLHDGPFKTPPEGPQAPRLNQSQVLFQHWARWGKWNKYQPLDHVRRYFGEKVALYFA	348	
		:     : :    : :  : :  :    :    :    :		
Db	119	AAYPELHDGDY-----NGENVEFNDRLLYEEWARYGVFYKYQPIDLVRKYFGEKIGLYFA	173	
Qy	349	WLGfYTGWLLPAAVVGTLVFLVGCFLVFSDIPTQELCGSKDSFEMCPLC-LDCPFWLLSS	407	
		: : :  :       : : :   :  : :        :  :		
Db	174	WLGvYTQMLIPASIVGIIVFLYGCATMDENIPSMEMCDQRHNITMCPLCDKTCsYWKMSs	233	
Qy	408	ACALAQAQARLFDHGGTVFFSLFMALWAVLLLEYWKRKSATLAYRWDCSDYEDTEE----R	463	
		:     :     :      : :            : : :		
Db	234	ACATARASHLFDNPATVFFSVFMALWAATFMEHWKRKQMRNLNYRWDLTGFEeeeeEAVKDH	293	

Qy 464 PRPQFAA-----SAPMTAPNPITGEDEPYFPERSRARRMLAGSVVIVVMVAVVVMCLVSI 518  
| | : : | | : | | : | | | : | : | : : :  
Db 294 PRAEYEARVLEKSLKKESRNKET--DKVKLTWRDRFPAYLTNLVSIIFMIAVTFAIVLGV 351

Qy 519 ILYRAIMAIVVSRSGNTLLAAWASRIASLTGSVVNLVFIILISKIYVSLAHVLTRWEMHR 578  
| : | | | : : : : : : : | : : | | : : | : | : : :  
Db 352 ILYRISMAAALAMNSSPSVRSNIRVTVTATAVIINLVVIILLDEVYGCARWLTKIEVPK 411

Qy 579 TQTKFEDAFTLKVFIFQFVNIFYSSPVYIAFFKGRFVGYPGNYHTLF-GVRNEECAAGGCL 637  
| : | | : | | : : | | : | : | | | | | | | : | : | | | | | | |  
Db 412 TEKSFEERLIFKAFLKLFVNSYTPIFYVAFFKGRFVGRPGDYVYIFRSFRMEECAPGGCL 471

Qy 638 IELAQELLVIMVGKQVI--NNMQEVLIPKLKGWWQKFRRLRSKKRKAGASAGASQGPWEDDY 696  
: | | : | : | : | | : | | : | | : | : : : : : : : : : : :  
Db 472 MELCIQLSIIMLGKQLIQNNLFEIGIPKMKKLIRYLKLKQQSPPDHEECVKKRQRYEVDY 531

Qy 697 ELVPCEGLFDEYLEMVLQFGFVTIFVAACPLAPLFAALLNNWVEIRLDARKFVCEYRRPVA 756  
| | | | : | : : | | : | : | : | : | : | : | : | : | : | : |  
Db 532 NLEPFAGLTPEYMEMIIQFGFVTLFVASFPLAPLFAALLNNIIEIRLDAKKFVTELRRPVA 591

Qy 757 ERAQDIGIWFHILAGLTHLAVISNAFLAFSSDFLPRA--YYRWTRAHDLRGFLNFTLAR 814  
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :  
Db 592 VRAKDIGIWNILRGIGKLAVIINAFVISFTSDFIPRLVYLYMYSKNGTMHGfVNHTL-- 649

Qy 815 APSSF-----AAAHN-----RTCRYRAFRD---DDGHY--SQTYWNLLAIRLAF 853  
| | | | : | :  
Db 650 --SSFNVSDFQNGTAPNDPLDLGYEVQICRYKDYREPPWSENKYDISKDFWAVLAARLAF 707

Qy 854 VIVFEHVVSFVGRLLDLLVPDIPESVEIKVKREYYLA-----KQALAENEVLFGT 903  
| | | : : : | : : : | : : | : : : : : : : : : : : : : : : :  
Db 708 VIVFQNLVFMFMSDFVDWVIPDIPKDISQQIHKEKVLMLVELFMREEQDKQQLL--ETWMEK 765

Qy 904 NGTKDEQP-----KGSELSSH 919  
| | | | | :  
Db 766 ERQKDEPPC�HHNTKACPDNLGSPAPSH 793

Search completed: October 1, 2008, 13:00:05

Job time : 830 secs

SCORE 3.3